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(21) International Application Number: PCT/US98/04610 (22) International Filing Date: 10 March 1998 (10.03.98) (30) Priority Data: 60/040,795 14 March 1997 (14.03.97) US (71) Applicant (for all designated States except US): MERCK & CO., INC. [US/US]; 126 East Lincoln Avenue, Rahway, NJ 07065 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): HERMES, Jeffrey, D. [US/US]; 126 East Lincoln Avenue, Rahway, NJ 07065 (US). SALOWE, Scott, P. [US/US]; 126 East Lincoln Avenue, Rahway, NJ 07065 (US). SINCLAIR, Peter, J. [US/US]; 126 East Lincoln Avenue, Rahway, NJ 07065 (US). (74) Common Representative: MERCK & CO., INC.; 126 East Lincoln Avenue, Rahway, NJ 07065 (US).	(81) Designated States: CA, JP, US, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>	
(54) Title: A HIGH THROUGHPUT ASSAY USING FUSION PROTEINS (57) Abstract This application describes a high throughput assay for screening compounds which are capable of binding to a fusion protein which consists of a target protein and an FK506-binding protein. This application also describes an assay for screening compounds which inhibit a protease.		

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TITLE OF THE INVENTION

A HIGH THROUGHPUT ASSAY USING FUSION PROTEINS

BACKGROUND OF THE INVENTION

5 Several assays have been developed that screen compounds to determine if they are capable of binding to a fusion protein. One such method uses heterobifunctional cross-linking with diamino-europium-cryptate and a protein of interest. However, the activity of the protein is often affected by the modification with the
10 heterobifunctional cross-linking agents. These methods also require an additional purification for the heterogeneous products resulting from the covalent modifications of the proteins.

A new method, Homogeneous Time-Resolved Fluorescence (HTRF), combines the benefits of a fluorescent label and a homogeneous
15 assay protocol in a high throughput screen. HTRF uses a pair of chemically stable labeling molecules, such as a lanthanide cryptate and a fluorescent molecule. Specifically, europium cryptate (Eu(K)) and XL-665 have been used to label biomolecules. XL-665 is a cross-linked derivative of allophycocyanin, a red-green algae pigment. HTRF works
20 by measuring the change in fluorescent energy. If XL-665 is in proximity to Eu(K), it will yield an amplified and long-lived signal. The amount of energy transfer is a function of proximity of the two molecules. Eu(K) has a long-lived fluorescent signal which facilitates the homogeneous nature of the assay. A time delay in reading the signal
25 eliminates the principal difficulty in applying fluorescence to screening formats. This technology is useful in both binding and protease assays. [Kolb et al., J. of Biomolecular Screening, 1, No. 4, 203-210 (1996); Kolb et al., Pharm. Manuf. Int., p. 31 (1996)]

SUMMARY OF THE INVENTION

30 The instant invention relates to a method of screening that can be used to determine if compounds are capable of binding to a protein or are capable of blocking ligand-protein or protein-protein interactions. The instant invention covers a method of screening for

compounds capable of binding to a fusion protein which comprises combining a test compound, a biotinylated ligand, a fusion protein (target protein, peptide linker and FK506-binding protein), a donor-labeled ligand, and acceptor-labeled streptavidin, and then measuring the fluorescence attributable to the binding of the biotinylated ligand to the fusion protein in the presence of the test compound relative to a control assay in the absence of the test compound, so as to determine the effect the test compound has on the binding of the biotinylated ligand. The instant invention also covers a method of screening for compounds which inhibit a protease which comprises combining a test compound, a fusion protein substrate (reporter protein, peptide linker and FK506-binding protein), a protease, a donor-labeled ligand, and acceptor-labeled streptavidin, and then measuring the fluorescence attributable to the binding of the intact fusion protein substrate in the presence of the test compound relative to a control assay in the absence of the test compound, so as to determine the effect the test compound has on proteolytic activity. This invention provides an immediate means of making use of HTRF technology for the functional assay of either ligand binding to a single or multiple signal transduction domain(s), tyrosine phosphatases, nuclear receptors or bacterial tRNA synthetases in a signal increase assay or proteolytic activity in a signal decrease assay. The present invention is readily adaptable to robotic automation for high capacity screening for agonists, antagonists, and/or inhibitors.

BRIEF DESCRIPTION OF THE FIGURES

FIGURE 1: Binding of the donor-labeled ligand (Eu(K) labeled ligand for FKBP), fusion protein (FKBP:SH2), biotinylated ligand and the acceptor-labeled streptavidin (SA-XL665), which involves a fluorescent energy transfer that can be measured.

FIGURE 2: Cleaving of donor-labeled ligand (Eu(K) labeled ligand for FKBP), fusion protein substrate (FKBP:SH2:ITAM:B) and the acceptor-labeled streptavidin (SA-XL665).

FIGURE 3: Cleaving of donor-labeled ligand (Eu(K) labeled ligand for FKBP), fusion protein substrate (FKBP:acetyl-CoA:B) and the acceptor-labeled streptavidin (SA-XL665).

5

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to a method of screening for compounds which preferentially bind to a target protein or inhibit a protease.

10

As depicted in Figure 1, an embodiment of this invention is a method of screening for compounds capable of binding to a fusion protein which comprises the steps of:

15

- a) mixing a test compound, a biotinylated ligand, the fusion protein, a donor-labeled ligand and acceptor-labeled streptavidin;
- b) incubating the mixture for an appropriate time;
- c) measuring the time-resolved fluorescence attributable to the binding of the biotinylated ligand to the fusion protein in the presence of the test compound; and
- 20 d) determining the binding of the biotinylated ligand to the fusion protein in the presence of the test compound relative to a control assay run in the absence of the test compound.

25

As depicted in Figures 2 and 3, another embodiment of this invention is a method of screening for compounds capable of inhibiting a protease which comprises the steps of:

30

- a) mixing a test compound, a fusion protein substrate, a donor-labeled ligand, acceptor-labeled streptavidin, and a protease;
- b) incubating the mixture for an appropriate time;
- c) measuring the time-resolved fluorescence attributable to the binding of the intact fusion protein substrate to the acceptor-labeled streptavidin in the presence of the test compound; and

- d) determining the binding of the intact fusion protein substrate to the acceptor-labeled streptavidin in the presence of the test compound relative to a control assay run in the absence of the test compound.

5

For Figures 1-3, the following definitions apply to the terms used therein:

- Eu(K) = Europium Cryptate
10 "506" = FK506 analog
FKBP = FK506 Binding Protein
SH2 = Src homology domain 2
12-mer = phosphotyrosine-containing, 12 peptide
B = biotin
15 (SH2)₂ = tandem SH2 domains of ZAP70
ITAM = bisphosphotyrosine-containing, 25 residue peptide
SA = streptavidin

The term "fusion protein" refers to a "target protein" fused
20 to an "FK506-binding protein" (FKBP), the two proteins being separated by a "peptide linker". The term "fusion protein substrate" refers to a "reporter protein" fused to an FKBP, the two proteins being separated by a peptide linker.

A "peptide linker" may consist of a sequence containing
25 from about 1 to about 20 amino acids, which may or may not include the sequence for a protease cleavage site. An example of a peptide linker which is a protease cleavage site is represented by the amino acid sequence GLVPRGS. (SEQ. ID. NO. 1).

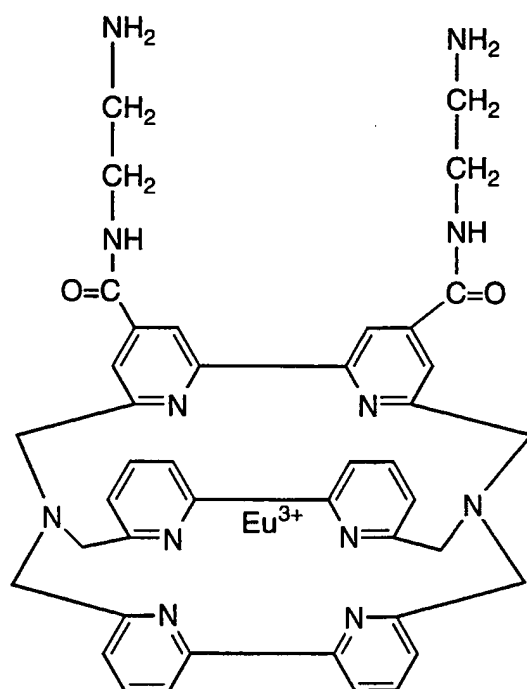
The term "protease" refers to an enzyme that catalyzes the
30 hydrolytic breakdown of proteins and/or peptides. Examples of proteases may include, but are not limited to, thrombin, Human Immunodeficiency Virus (HIV) protease and Tumor Necrosis Factor (TNF) α converting enzyme.

The term "target protein" refers to any protein that has a defined ligand. Types of target proteins include, but are not limited to, tyrosine phosphatases (FKBP-phosphatase chimera as receptor and biotinylated-peptide containing a phosphonomethylene isostere as ligand), nuclear
5 receptors (FKBP-receptor and biotinylated DNA) and bacterial tRNA synthetases (FKBP-tRNA synthetase and biotinylated tRNA). Also included within this definition of target protein are single and multiple signal transduction domains, such as, but not limited to, Src homology 1 (SH1), Src homology 2 (SH2), Src homology 3 (SH3), and pleckstrin
10 homology (PH) domains [Hanks & Hunter, *FASEB J.*, 9, 576-596 (1995); Bolen, *Curr. Opin. Immunol.*, 7, 306-311 (1995); Kuriyan & Cowburn, *Curr. Opin. Struct. Biol.*, 3, 828-837 (1993); Cohen et al., *Cell*, 80, 237-248 (1995)]. The term "SH1 domain" refers to a family of homologous protein domains that bind ATP and catalyze tyrosine
15 phosphorylation of peptide and protein substrates. The term "SH2 domain" refers to a family of homologous protein domains that share the common property of recognizing phosphorylated tyrosine residues in specific peptide contexts. The term "SH3 domain" refers to a family of homologous protein domains that share the common property of
20 recognizing polyproline type II helices. The term "PH domain" refers to a family of homologous protein domains that mediate both protein-protein and protein-lipid interactions. Examples of SH2 domains which may be utilized in the method of the invention include, but are not limited to, the single and tandem SH2 domains present in the tyrosine
25 kinases ZAP70, Syk and Lck. The DNA sequences were obtained from GenBank, National Center for Biotechnology Information, National Library of Medicine, 8600 Rockville Pike, Bethesda, MD 20894. The Accession Numbers for the sequences are: human ZAP70 (L05148) human Syk (L28824) and human Lck (X13529). The sequences for
30 ZAP70, Syk and Lck are disclosed in the sequence listing as follows: the isolated DNA encoding for a fusion protein containing ZAP70 is (SEQ. ID. NO. 2); the isolated DNA encoding for a fusion protein containing Syk is (SEQ. ID. NO. 3); the isolated DNA encoding for a fusion protein containing Lck is (SEQ. ID. NO. 4); the sequence for the

FKBP-ZAP70:SH2 fusion protein is (SEQ. ID. NO. 5); the sequence for the FKBP-Syk:SH2 fusion protein is (SEQ. ID. NO. 6); and the sequence for the FKBP-Lck:SH2 fusion protein is (SEQ. ID. NO. 7).

5 The term "reporter protein" refers to a protein containing covalent biotin or a noncovalently bound biotinylated ligand. Examples of proteins containing covalent biotin are the C-terminal 87 residues of the biotin carboxy carrier protein of acetyl-CoA carboxylase from *Escherichia coli* and the biotin-carrier subunit of transcarboxylase from *Propionibacterium shermanii*. An example of a protein containing a
10 noncovalently bound biotinylated ligand is the tandem SH2 domains of ZAP70 bound to a biotinylated phosphopeptide derived from an Immunoreceptor Tyrosine-based Activation Motif (ITAM) sequence of the human T-cell receptor, the B-cell receptor or a high affinity Immunoglobulin E. (IgE) receptor. Specifically, the Zeta (ζ) 1
15 sequence of the human T-cell receptor may be utilized. (SEQ. ID. NO. 8) (California Peptide Research Inc., 918 Enterprise Way, Suite 1, Napa, CA 94558)

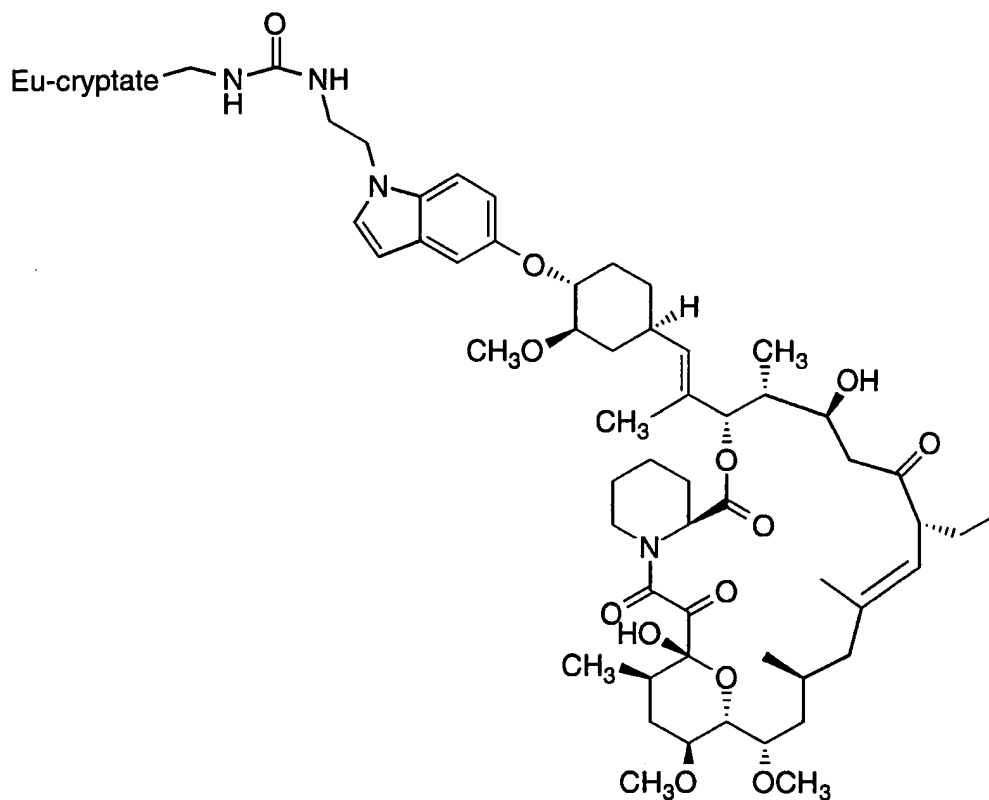
20 The term "donor-labeled ligand" refers to an organic cryptate-containing molecule loaded with a fluorescent lanthanide metal which binds to the FKBP. An example of a fluorescent lanthanide metal is europium. The europium-cryptate molecule was obtained from CIS Bio International, Subsidiary of Compagnie ORIS INDUSTRIE SA, Boite Postale 175, F30203 Bagnols sur Ceze Cedex, France, is depicted below.



5

Europium Cryptate (Eu(K))

An example of a donor-labeled ligand useful in the instant invention is



The term "acceptor-labeled streptavidin" refers to streptavidin coupled to one or more light harvesting molecules. An example of a light harvesting molecule is allophycocyanin and an example of a acceptor-labeled streptavidin useful in the instant invention is SA-XL665. (CIS Bio International, Subsidiary of Compagnie ORIS INDUSTRIE SA, Boite Postale 175, F30203 Bagnols sur Ceze Cedex, France)

The term "control assay" refers to the assay when performed in the presence of the donor-labeled ligand, acceptor-labeled streptavidin, and either fusion protein substrate or fusion protein plus biotinylated ligand, but in the absence of the test compound.

The term FK506-binding proteins may include, but are not limited to, the below listed FKBP's and FKBP homologues, which

include a citation to the references which disclose them. This list is not intended to limit the scope of the invention.

Mammalian

- | | | |
|----|-----------|--|
| 5 | FKBP-12 | Galat et al., <i>Eur. J. Biochem.</i> , 216:689-707 (1993). |
| | FKBP-12.6 | Wiederrecht, G. and F. Etzkorn
<i>Perspectives in Drug Discovery and Design</i> , 2:57-84 (1994). |
| 10 | FKBP-13 | Galat et al., <i>supra</i> ; Wiederrecht and Etzkorn, <i>supra</i> . |
| | FKBP-25 | Galat et al., <i>supra</i> ; Wiederrecht and Etzkorn, <i>supra</i> . |
| | FKBP-38 | Wiederrecht and Etzkorn, <i>supra</i> . |
| 15 | FKBP-51 | Baughman et al., <i>Mol. Cell. Biol.</i> , 8, 4395-4402(1995) . |
| | FKBP-52 | Galat et al., <i>supra</i> . |

Bacteria

- | | | |
|----|---------------------------|---|
| 20 | Legionella pneumophila | Galat et al., <i>supra</i> . |
| | Legionella micadei | Galat et al., <i>supra</i> . |
| | Chlamydia trachomatis | Galat et al., <i>supra</i> . |
| | E. coli fkpa | Horne, S.M. and K.D. Young, <i>Arch. Microbiol.</i> , 163:357-365 (1995). |
| 25 | E. coli slyD | Roof et al., <i>J. Biol. Chem.</i> 269:2902-2910 (1994). |
| | E. coli orf149 | Trandinh et al., <i>FASEB J.</i> 6:3410-3420 (1992). |
| | Neisseria meningitidis | Hacker, J. and G. Fischer, <i>Mol. Micro.</i> , 10:445-456 (1993). |
| 30 | Streptomyces chrysomallus | Hacker and Fischer, <i>supra</i> . |

Fungal

- | | | |
|---|------------------|---|
| | yeast FKBP-12 | Cardenas et al., <i>Perspectives in Drug Discovery and Design</i> , 2:103-126 (1994). |
| 5 | yeast FKBP-13 | Cardenas et al., <i>supra</i> . |
| | yeast NPR1(FPR3) | Cardenas et al., <i>supra</i> . |
| | Neurospora | Galat et al., <i>supra</i> . |

A variety of host cells used to produce the FKBP
 10 chimeras may be used in this invention, which include, but are not limited to, bacteria, yeast, bluegreen algae, plant cells, insect cells and animal cells.

Expression vectors are defined herein as DNA sequences that are required for the transcription of cloned copies of genes and
 15 the translation of their mRNAs in an appropriate host. Such vectors can be used to express genes in a variety of host cells, such as, bacteria, yeast, bluegreen algae, plant cells, insect cells and animal cells.

Specifically designed vectors allow the shuttling of DNA
 20 between hosts such as bacteria-yeast or bacteria-animal cells. An appropriately constructed expression vector may contain: an origin of replication for autonomous replication in host cells, selectable markers, a limited number of useful restriction enzyme sites, a potential for high copy number, and active promoters. A promoter is defined as a DNA
 25 sequence that directs RNA polymerase to bind to DNA and initiate RNA synthesis. A strong promoter is one which causes mRNAs to be initiated at high frequency. Expression vectors may include, but are not limited to, cloning vectors, modified cloning vectors, specifically designed plasmids or viruses. Commercially available vectors suitable for FKBP
 30 fusion protein expression include, but are not limited to pBR322 (Promega), pGEX (Amersham), pT7 (USB), pET (Novagen), pIBI (IBI), pProEX-1 (Gibco/BRL), pBluescript II (Stratagene), pTZ18R and pTZ19R (USB), pSE420 (Invitrogen), pVL1392 (Invitrogen), pBlueBac (Invitrogen), pBacPAK (Clontech), pHIL (Invitrogen), pYES2

(Invitrogen), pCDNA (Invitrogen), pREP (Invitrogen) or the like. The expression vector may be introduced into host cells via any one of a number of techniques including but not limited to transformation, transfection, infection, protoplast fusion, and electroporation.

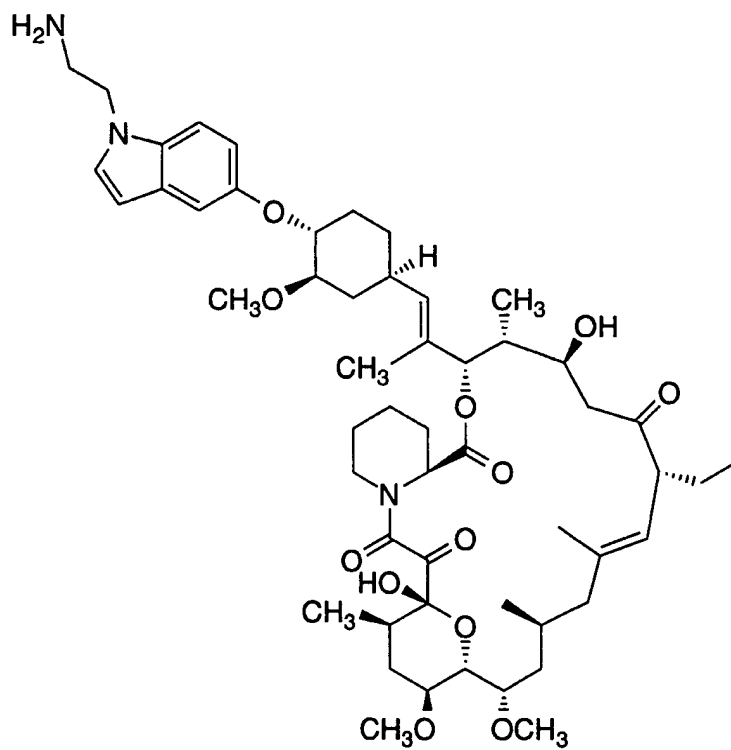
5 *E. coli* containing an expression plasmid with the gene for the target or reporter protein fused to FKBP are grown and appropriately induced. The cells are then pelleted and resuspended in a suitable buffer. Although FKBP-12 lacks sequences that specifically direct it to the periplasm, FKBP fusions may be located there and can be
10 released by a standard freeze/thaw treatment of the cell pellet. Following centrifugation, the resulting supernatant contains >80% pure FKBP fusion, which if desired can be purified further by conventional methods. Alternatively, the assay is not dependent on pure protein and the initial periplasmic preparation may be used directly.

15 A fusion protein which contains a single or multiple SH2 domain(s) may be purified by preparing an affinity matrix consisting of biotinylated phosphopeptide coupled to avidin or streptavidin immobilized on a solid support. A freeze/thaw extract is prepared from the cells which express the fusion protein and is loaded onto the affinity
20 matrix. The desired fusion protein is then specifically eluted with phenyl phosphate.

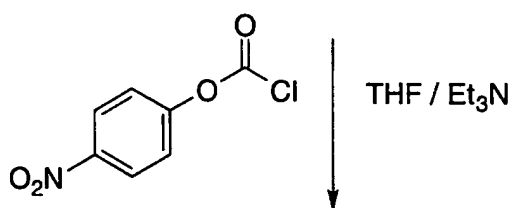
 To assay the formation of a complex between a target protein and its ligand, the biotinylated ligand is mixed with the FKBP fusion protein in a suitable buffer in the presence of the donor-labeled
25 ligand in the well of a black microplate. After a suitable incubation period to allow complex formation to occur, acceptor-labeled streptavidin is added to capture the tagged ligand and any bound fusion protein. The plate is incubated for a sufficient period to allow the capture to go to completion and then the time resolved fluorescent signal
30 is measured. Screening for agonists/antagonists/inhibitors is carried out by performing the initial incubation prior to the acceptor-labeled streptavidin capture step in the presence of a test compound(s) to determine whether they have an effect upon the binding of the

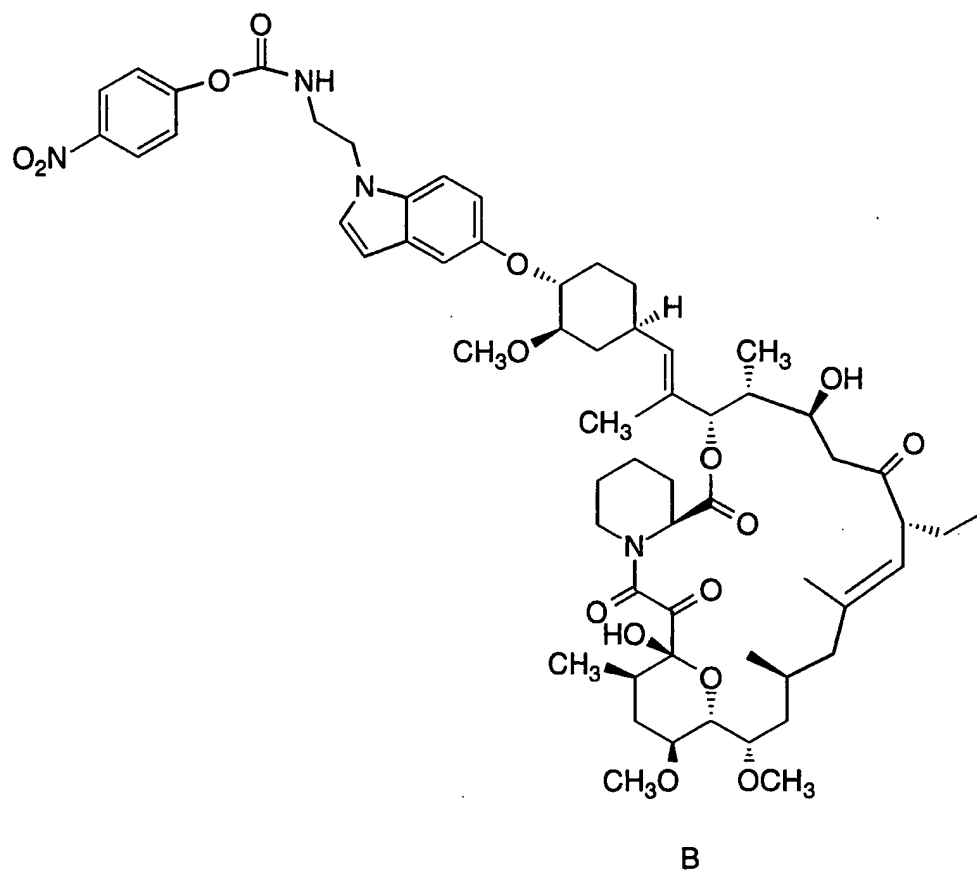
biotinylated ligand to the fusion protein. This principle is illustrated by Figure 1.

5 To assay the catalytic activity of a protease, a FKBP fusion protein substrate is combined with the protease in a suitable buffer in the presence of the donor-labeled ligand and acceptor-labeled streptavidin in the well of a black microplate. After a suitable incubation period, the time resolved fluorescent signal of the remaining intact fusion protein substrate is measured. Screening for inhibitors is carried out by performing the incubation in the presence of a test
10 compound(s) to determine whether they have an effect upon the cleavage of the fusion protein substrate. This principle is illustrated by Figures 2 and 3.

SCHEME 1

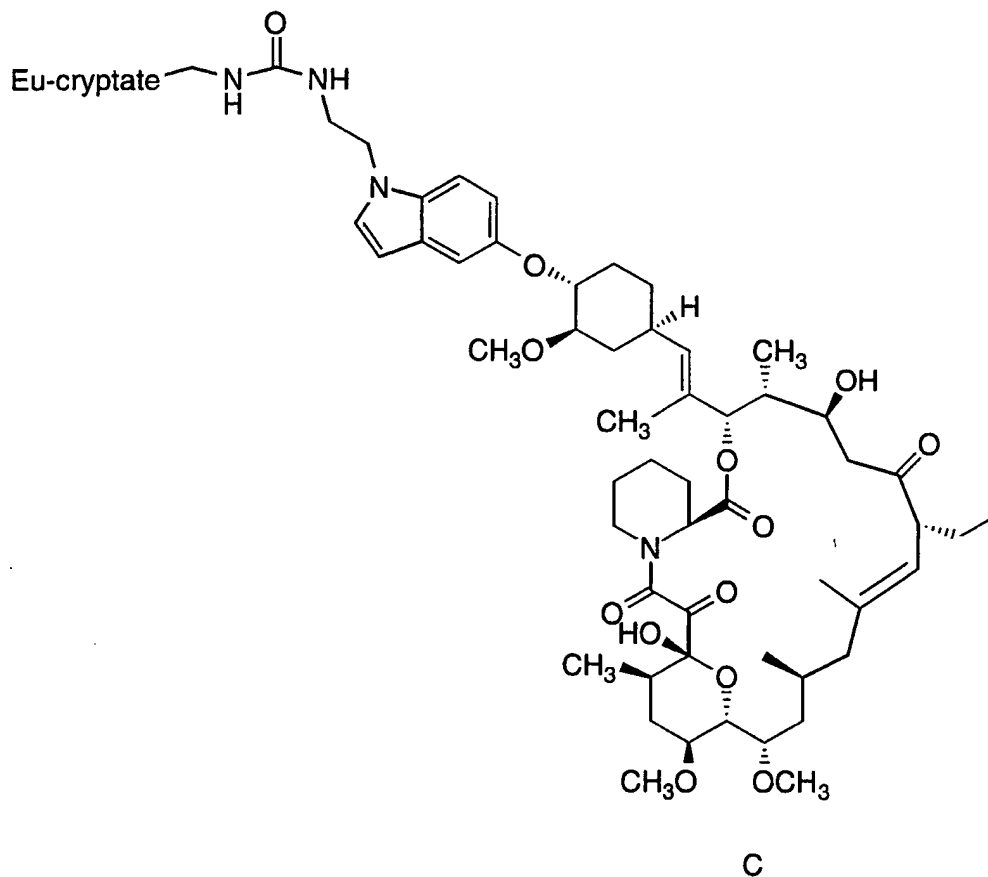
A



SCHEME 1 (cont'd.)

Eu-cryptate-NH₂ THF / Et₃N



SCHEME 1 (cont'd.)

5

Scheme 1 depicts the treatment of Compound A, an analog of FK506, with 1 equivalent of p-nitrophenylchloroformate in THF in the presence of a tertiary amine, which gives the p-nitrophenylcarbamate, Compound B. The nitrophenylcarbamate is isolated by silica gel chromatography or used without further purification. The nitrophenylcarbamate is an activated acylating group and will undergo attack by a variety of nucleophiles. The cryptate has two primary amino groups (nucleophiles). Treatment of the p-nitrophenylcarbamate with the europium cryptate in a non-protic

solvent (such as THF) in the presence of a tertiary amine should afford the corresponding urea. Compound C, the cryptate hybrid of the FK506 analog, will be purified by either normal phase silica gel chromatography on prep TLC plates or by reverse phase HPLC chromatography.

The cryptate can be linked to Compound A, other FK506 analogs, and related molecules by a variety of linkages, such as carbamates, amides, ureas, amines, etc. One of ordinary skill in the art would be familiar with the standard procedures used to prepare the FK506 analog containing the cryptate molecule.

The present invention can be understood further by the following examples, which do not constitute a limitation of the invention.

EXAMPLE 1

Process for Preparing the FKBP fusion cloning vector

General techniques for modifying and expressing genes in various host cells can be found in Ausubel, F.M., Brent, R., Kingston, R.E., Moore, D.D., Seidman, J.G., Smith, J.A. and Struhl, K. Current Protocols in Molecular Biology (John Wiley & Sons, New York, New York, 1989). Sequences for a 3'- altered FKBP fragment that contained a glycine codon (GGT) in place of the stop (TGA) codon followed by a sequence encoding a thrombin site (Leu-Val-Pro-Arg) and *Bam*HI restriction site (GGATCC) were amplified using the polymerase chain reaction (PCR). The PCR reaction contained the following primers: 5'-GATCGCCATGGGAGTGCAGGTGGAAACCATCTCCCCA-3' (SEQ. ID. NO. 9) and 5'-TACGAATTCTGGCGTGGATCCAC GCGGAACCAGACCTTCCAGTTTGTAG-3' (SEQ. ID. NO. 10) and a plasmid containing human FKBP-12 as the template. The resulting 367 base pair amplification product was ligated into the vector pCRII (Invitrogen) and the ligation mixture transformed into competent *Escherichia coli* cells. Clones containing an insert were identified using PCR with flanking vector primers. Dideoxy DNA sequencing confirmed the nucleotide sequence of one positive isolate. The altered

- 338 base pair FKBP fragment was excised from the pCRII plasmid using *NcoI* and *BamHI* and ligated into *NcoI* and *BamHI* digested pET9d (Novagen) plasmid. Competent *E. coli* were transformed with the ligation mixture, and colonies containing the insert were identified using
- 5 PCR with primers encoding for flanking vector sequences. The FKBP fusion cloning vector is called pET9dFKBPt.

EXAMPLE 2

10 Process for Preparing the FK-ZAP70 fusion expression vector

- A DNA fragment encoding for the tandem SH2 domains of ZAP70 was prepared by PCR to contain a *BamHI* site at the 5'-end such that the reading frame was conserved with that of FKBP in the fusion vector. At the 3'-end, the fragment also incorporated a stop codon
- 15 followed by a *BamHI* site. The PCR reaction contained Molt-4 cDNA (Clontech) and the following primers:
5'-ATTAGGATCCATGCCAGATCCTGCAGCTCACCTGCCCT-3'
(SEQ. ID. NO. 11) and 5'-ATATGGATCCTTACCAGAGGCGTTGCT-3'
(SEQ. ID. NO. 12). The fragment was cloned into a suitable vector,
- 20 sequenced, digested with *BamHI*, and the insert containing the SH2 domains ligated to *BamHI* treated pET9dFKBPt, and transformed into *E. coli*. Clones containing inserts in the correct orientation were identified by PCR or restriction enzyme analysis. Plasmid DNA was prepared and used to transform BL21(DE3) cells.

25

EXAMPLE 3

Process for Preparing the FK-Syk fusion expression vector

- The expression vector for the tandem SH2 domains of Syk fused to FKBP was prepared as in Example 2 except that the PCR
- 30 reaction contained Raji cell cDNA (Clontech) and the following primers: 5'-CAATAGGATCCATGGCCAGCAGCGGCATGGCTGA-3'
(SEQ. ID. NO. 13) and
5'-GACCTAGGATCCCTAATTAACATTTCCCTGTGTGCCGAT-3'
35 (SEQ. ID. NO. 14).

EXAMPLE 4

Process for Preparing the FK-Lck fusion expression vector

- 5 The expression vector for the SH2 domain of Lck fused to FKBP was prepared as in Example 2 except that the PCR reaction contained Molt-4 cDNA (Clontech) and the following primers:
- 5'-ATATGGATCCATGGCGAACAGCCTGGAGCCCCGAACCCT-3'
 (SEQ. ID. NO. 15) and
- 10 5'-ATTAGGATCCTTAGGTCTGGCAGGGGCGGCTCAACCGTGT
 GCA-3' (SEQ. ID. NO. 16).

EXAMPLE 5

FK-ZAP70

- 15 Step A: Process for Expression of FK-ZAP70
- E. coli* BL21(DE3) cells containing the pET9dFKBPt/
ZAP70SH2 plasmid were grown in Luria-Bertani (LB) media
containing 50 microgram/ml kanamycin at 37 degrees C until the optical
20 density measured at 600 nm was 0.5-1.0. Expression of the FK-ZAP70
fusion protein was induced with 0.1 mM isopropyl beta-
thiogalactopyranoside and the cells were grown for another 3-5 hr at 30
degrees C. They were pelleted at 4400 x g for 10 min at 4 degrees C
and resuspended in 2% of the original culture volume with 100 mM tris
25 pH 8.0 containing 1 microgram/ml each aprotinin, pepstatin, leupeptin,
and bestatin. The resuspended pellet was frozen at -20 degrees C until
further purification.
- Step B: Process for Purification of FK-ZAP70
- 30 The affinity matrix for purification of FK-ZAP70 was
prepared by combining agarose-immobilized avidin with excess
biotinylated phosphopeptide derived from the ζ 1 ITAM sequence of the
human T-cell receptor, biotinyl-GSNQLpYNELNLGRREEpYDVLDK,
(SEQ. ID. NO. 8) and washing out unbound peptide. Frozen cells
35 containing FK-ZAP70 were thawed in warm water, refrozen on dry ice

for about 25 min., then thawed again. After the addition of 0.1% octyl glucoside, 1 mM dithiothreitol (DTT) and 500 mM NaCl, the extract was centrifuged at 35,000 x g for approximately 30 minutes. The supernatant was loaded onto the phosphopeptide affinity column, at about 4° and washed with phosphate buffered saline containing 1 mM DTT and 0.1% octyl glucoside. FK-ZAP70 was eluted with 200 mM phenyl phosphate in the same buffer at about 37°. The protein pool was concentrated and the phenyl phosphate removed on a desalting column. The purified FK-ZAP70 was stored at about -30° in 10 mM HEPES/150 mM NaCl/1 mM DTT/0.1 mM EDTA/10% glycerol.

EXAMPLE 6

FK-Syk

E. coli BL21(DE3) cells containing the pET9dFKBPt/SykSH2 plasmid were grown, induced, and harvested as described in Example 5. FK-Syk was purified using the same affinity matrix and methodology described in Example 5.

EXAMPLE 7

FK-Lck

E. coli BL21(DE3) cells containing the pET9dFKBPt/LckSH2 plasmid were grown, induced, and harvested as described in Example 5. The affinity matrix for purification of FK-Lck was prepared by combining agarose-immobilized avidin with excess biotinyl-EPQpYEEIPIYL, (SEQ. ID. NO. 17) and washing out unbound peptide. The remaining methodology for purification was the same as Example 5.

EXAMPLE 8

Method of Screening for Inhibitors of FK-ZAP

A DMSO solution of test compound(s) and biotinyl-phosphopeptide stock solution in a suitable buffer are dispensed into the

- wells of a 96-well black microplate. Next, a mixture of FK-ZAP protein and Eu(K)-labeled FK506 analog are added to each test well. Finally, a solution of SA-XL665 is dispensed to each well and the plate is incubated for an appropriate time. The fluorescence ratio is then
- 5 measured in a Packard Discovery HTRF analyzer. (Packard Instrument Company, 800 Research Parkway, Meridan, CT 06450)

EXAMPLE 9

10 Method of Screening for Inhibitors of Thrombin

- A DMSO solution of test compound(s) and a suitable buffer containing a mixture of FK-ZAP protein, Eu(K)-labeled FK506 analog, and biotinyl-phosphopeptide are dispensed into the wells of a 96-well black microplate. Next, thrombin is added to each test well. After an
- 15 appropriate incubation period, a solution of SA-XL665 is dispensed to each well. The fluorescence ratio is then measured in a Packard Discovery HTRF analyzer. (Packard Instrument Company, 800 Research Parkway, Meridan, CT 06450)

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: HERMES, JEFFREY D.
SALOWE, SCOTT P.
SINCLAIR, PETER J.
- (ii) TITLE OF THE INVENTION: A HIGH THROUGHPUT ASSAY USING
FUSION PROTEINS
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Merck & Co., Inc.
 - (B) STREET: P.O. Box 2000, 126 E. Lincoln Ave.
 - (C) CITY: Rahway
 - (D) STATE: NJ
 - (E) COUNTRY: USA
 - (F) ZIP: 07065-0900
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/040,795
 - (B) FILING DATE: 14 March 1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Camara, Valerie J
 - (B) REGISTRATION NUMBER: 35,090
 - (C) REFERENCE/DOCKET NUMBER: 19916
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 732-594-3902
 - (B) TELEFAX: 732-594-4720
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Gly Leu Val Pro Arg Gly Ser
 1 5

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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ATGGGAGTGC AGGTGGAAAC CATCTCCCCA GGAGATGGAC GCACCTTCCC CAAGCGCGGC 60
CAGACCTGCG TGGTGCACTA CACCGGGATG CTTGAAGATG GAAAGAAATT TGATTCCTCC 120
CGGGACAGAA ACAAGCCCTT TAAGTTTATG CTAGGCAAGC AGGAGGTGAT CCGAGGCTGG 180
GAAGAAGGGG TTGCCCAGAT GAGTGTGGGT CAGAGAGCCA AACTGACTAT ATCTCCAGAT 240
TATGCCATATG GTGCCACTGG GCACCCAGGC ATCATCCCAC CACATGCCAC TCTCGTCTTC 300
GATGTGGAGC TTCTAAAACT GGAAGGTCTG GTTCCGCGTG GATCCATGCC AGATCCTGCA 360
GCTCACCTGC CCTTCTTCTA CGGCAGCATC TCGCGTGCCG AGGCCGAGGA GCACCTGAAG 420
CTGGCGGGCA TGGCGGACGG GCTCTTCCTG CTGCGCCAGT GCCTGCGCTC GCTGGGCGGC 480
TATGTGCTGT CGCTCGTGCA CGATGTGCGC TTCCACCAC TTTCCCATCGA GCGCCAGCTC 540
AACGGCACCT ACGCCATTGC CGGCGGCAA GCGCACTGTG GACCGGCAGA GCTCTGCGAG 600
TTCTACTCGC GCGACCCCGA CGGGCTGCCC TGCAACCTGC GCAAGCCGTG CAACCGGCCG 660
TCGGGCCTCG AGCCGCAGCC GGGGGTCTTC GACTGCCTGC GAGACGCCAT GGTGCGTGAC 720
TACGTGCGCC AGACGTGGA GCTGGAGGGC GAGGCCCTGG AGCAGGCCAT CATCAGCCAG 780
GCCCCGAGG TGGAGAAGCT CATTGCTACG ACGGCCCACG AGCGGATGCC CTGGTACCAC 840
AGCAGCCTGA CGCGTGAGGA GGCCGAGCGT AAACCTTTACT CTGGGGCGCA GACCGACGGC 900
AAGTTCCTGC TGAGGCCGCG GAAGGAGCAG GGCACATACG CCCTGTCCCT CATCTATGGG 960
AAGACGGTGT ACCACTACCT CATCAGCCAA GACAAGGCGG GCAAGTACTG CATTCCCGAG 1020
GGCACCAAGT TTGACACGCT CTGGCAGCTG GTGGAGTATC TGAAGCTGAA GCGCGACGGG 1080
CTCATCTACT GCCTGAAGGA GGCCTGCCCC AACAGCAGTG CCAGCAACGC CTCTTAA 1137

```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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ATGGGAGTGC AGGTGGAAAC CATCTCCCCA GGAGATGGAC GCACCTTCCC CAAGCGCGGC 60
CAGACCTGCG TGGTGCACTA CACCGGGATG CTTGAAGATG GAAAGAAATT TGATTCCTCC 120
CGGGACAGAA ACAAGCCCTT TAAGTTTATG CTAGGCAAGC AGGAGGTGAT CCGAGGCTGG 180
GAAGAAGGGG TTGCCCAGAT GAGTGTGGGT CAGAGAGCCA AACTGACTAT ATCTCCAGAT 240
TATGCCATATG GTGCCACTGG GCACCCAGGC ATCATCCCAC CACATGCCAC TCTCGTCTTC 300
GATGTGGAGC TTCTAAAACT GGAAGGTCTG GTTCCGCGTG GATCCATGGC CAGCAGCGGC 360

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ATGGCTGACA GCGCCAACCA CCTGCCCTTC TTTTTCGGCA ACATCACCCG GGAGGAGGCA 420
GAAGATTACC TGGTCCAGGG GGGCATGAGT GATGGGCTTT ATTTGCTGCG CCAGAGCCGC 480
AACTACCTGG GTGGCTTCGC CCTGTCCGTG GCCCACGGGA GGAAGGCACA CCACTACACC 540
ATCGAGCGGG AGCTGAATGG CACCTACGCC ATCGCCGGTG GCAGGACCCA TGCCAGCCCC 600
GCCGACCTCT GCCACTACCA CTCCCAGGAG TCTGATGGCC TGGTCTGCCT CCTCAAGAAG 660
CCCTTCAACC GGCCCCAAGG GGTGCAGCCC AAGACTGGGC CCTTTGAGGA TTTGAAGGAA 720
AACCTCATCA GGAATATGT GAAGCAGACA TGAACCTGC AGGGTCAGGC TCTGGAGCAG 780
GCCATCATCA GTCAGAAGCC TCAGCTGGAG AAGCTGATCG CTACCACAGC CCATGAAAAA 840
ATGCCTTGGT TCCATGGAAA AATCTCTCGG GAAGAATCTG AGCAAATTGT CCTGATAGGA 900
TCAAAGACAA ATGGAAAGTT CCTGATCCGA GCCAGAGACA ACAACGGCTC CTACGCCCTG 960
TGCGTGCTGC ACGAAGGGAA GGTGCTGCAC TATCGCATCG ACAAAGACAA GACAGGGAAG 1020
CTCTCCATCC CCGAGGGAAA GAAGTTCGAC ACGCTCTGGC AGCTAGTCGA GCATTATTCT 1080
TATAAAGCAG ATGGTTTGT AAGAGTTCTT ACTGTCCCAT GTCAAAAAAT CGGCACACAG 1140
GGAAATGTTA ATTAG                                     1155

```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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ATGGGAGTGC AGGTGGAAAC CATCTCCCA GGAGATGGAC GCACCTTCCC CAAGCGCGGC 60
CAGACCTGCG TGGTGCACTA CACCGGGATG CTTGAAGATG GAAAGAAATT TGATTCCTCC 120
CGGGACAGAA ACAAGCCCTT TAAGTTTATG CTAGGCAAGC AGGAGGTGAT CCGAGGCTGG 180
GAAGAAGGGG TTGCCCAGAT GAGTGTGGGT CAGAGAGCCA AACTGACTAT ATCTCCAGAT 240
TATGCCATATG GTGCCACTGG GCACCCAGGC ATCATCCAC CACATGCCAC TCTCGTCTTC 300
GATGTGGAGC TTCTAAAACT GGAAGGTCTG GTTCCGCGTG GATCCATGGC GAACAGCCTG 360
GAGCCCGAAC CCTGGTTCTT CAAGAACCTG AGCCGCAAGG ACGCGGAGCG GCAGCTCCTG 420
GCGCCCGGGA AACTCACGG CTCCTTCCTC ATCCGGGAGA GCGAGAGCAC CGCGGGATCG 480
TTTTCACTGT CGGTCCGGGA CTTGACCAG AACCAGGGAG AGGTGGTGAA ACATTACAAG 540
ATCCGTAATC TGGACAACGG TGGCTTCTAC ATCTCCCTC GAATCACTTT TCCCGGCTG 600
CATGAAGTGG TCCGCCATTA CACCAATGCT TCAGATGGGC TGTGCACACG GTTGAGCCGC 660
CCCTGCCAGA CCTAA                                     675

```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
 1           5           10           15
Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
          20           25           30

```

```

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
      35              40              45
Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
      50              55              60
Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
      65              70              75              80
Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
      85              90              95
Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Leu Val Pro
      100             105             110
Arg Gly Ser Met Pro Asp Pro Ala Ala His Leu Pro Phe Phe Tyr Gly
      115             120             125
Ser Ile Ser Arg Ala Glu Ala Glu Glu His Leu Lys Leu Ala Gly Met
      130             135             140
Ala Asp Gly Leu Phe Leu Leu Arg Gln Cys Leu Arg Ser Leu Gly Gly
      145             150             155             160
Tyr Val Leu Ser Leu Val His Asp Val Arg Phe His His Phe Pro Ile
      165             170             175
Glu Arg Gln Leu Asn Gly Thr Tyr Ala Ile Ala Gly Gly Lys Ala His
      180             185             190
Cys Gly Pro Ala Glu Leu Cys Glu Phe Tyr Ser Arg Asp Pro Asp Gly
      195             200             205
Leu Pro Cys Asn Leu Arg Lys Pro Cys Asn Arg Pro Ser Gly Leu Glu
      210             215             220
Pro Gln Pro Gly Val Phe Asp Cys Leu Arg Asp Ala Met Val Arg Asp
      225             230             235             240
Tyr Val Arg Gln Thr Trp Lys Leu Glu Gly Glu Ala Leu Glu Gln Ala
      245             250             255
Ile Ile Ser Gln Ala Pro Gln Val Glu Lys Leu Ile Ala Thr Thr Ala
      260             265             270
His Glu Arg Met Pro Trp Tyr His Ser Ser Leu Thr Arg Glu Glu Ala
      275             280             285
Glu Arg Lys Leu Tyr Ser Gly Ala Gln Thr Asp Gly Lys Phe Leu Leu
      290             295             300
Arg Pro Arg Lys Glu Gln Gly Thr Tyr Ala Leu Ser Leu Ile Tyr Gly
      305             310             315             320
Lys Thr Val Tyr His Tyr Leu Ile Ser Gln Asp Lys Ala Gly Lys Tyr
      325             330             335
Cys Ile Pro Glu Gly Thr Lys Phe Asp Thr Leu Trp Gln Leu Val Glu
      340             345             350
Tyr Leu Lys Leu Lys Ala Asp Gly Leu Ile Tyr Cys Leu Lys Glu Ala
      355             360             365
Cys Pro Asn Ser Ser Ala Ser Asn Ala Ser
      370             375

```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
 1           5           10           15
Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
 20           25           30
Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
 35           40           45
Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
 50           55           60
Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
 65           70           75           80
Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
 85           90           95
Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Leu Val Pro
 100          105          110
Arg Gly Ser Met Ala Ser Ser Gly Met Ala Asp Ser Ala Asn His Leu
 115          120          125
Pro Phe Phe Phe Gly Asn Ile Thr Arg Glu Glu Ala Glu Asp Tyr Leu
 130          135          140
Val Gln Gly Gly Met Ser Asp Gly Leu Tyr Leu Leu Arg Gln Ser Arg
 145          150          155          160
Asn Tyr Leu Gly Gly Phe Ala Leu Ser Val Ala His Gly Arg Lys Ala
 165          170          175
His His Tyr Thr Ile Glu Arg Glu Leu Asn Gly Thr Tyr Ala Ile Ala
 180          185          190
Gly Gly Arg Thr His Ala Ser Pro Ala Asp Leu Cys His Tyr His Ser
 195          200          205
Gln Glu Ser Asp Gly Leu Val Cys Leu Leu Lys Lys Pro Phe Asn Arg
 210          215          220
Pro Gln Gly Val Gln Pro Lys Thr Gly Pro Phe Glu Asp Leu Lys Glu
 225          230          235          240
Asn Leu Ile Arg Glu Tyr Val Lys Gln Thr Trp Asn Leu Gln Gly Gln
 245          250          255
Ala Leu Glu Gln Ala Ile Ile Ser Gln Lys Pro Gln Leu Glu Lys Leu
 260          265          270
Ile Ala Thr Thr Ala His Glu Lys Met Pro Trp Phe His Gly Lys Ile
 275          280          285
Ser Arg Glu Glu Ser Glu Gln Ile Val Leu Ile Gly Ser Lys Thr Asn
 290          295          300
Gly Lys Phe Leu Ile Arg Ala Arg Asp Asn Asn Gly Ser Tyr Ala Leu
 305          310          315          320
Cys Leu Leu His Glu Gly Lys Val Leu His Tyr Arg Ile Asp Lys Asp
 325          330          335
Lys Thr Gly Lys Leu Ser Ile Pro Glu Gly Lys Lys Phe Asp Thr Leu
 340          345          350
Trp Gln Leu Val Glu His Tyr Ser Tyr Lys Ala Asp Gly Leu Leu Arg
 355          360          365
Val Leu Thr Val Pro Cys Gln Lys Ile Gly Thr Gln Gly Asn Val Asn
 370          375          380

```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
 1           5           10           15
Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
 20           25           30
Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
 35           40           45
Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
 50           55           60
Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
 65           70           75           80
Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
 85           90           95
Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu Gly Leu Val Pro
100          105          110
Arg Gly Ser Met Ala Asn Ser Leu Glu Pro Glu Pro Trp Phe Phe Lys
115          120          125
Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro Gly Asn
130          135          140
Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser Thr Ala Gly Ser
145          150          155          160
Phe Ser Leu Ser Val Arg Asp Phe Asp Gln Asn Gln Gly Glu Val Val
165          170          175
Lys His Tyr Lys Ile Arg Asn Leu Asp Asn Gly Gly Phe Tyr Ile Ser
180          185          190
Pro Arg Ile Thr Phe Pro Gly Leu His Glu Leu Val Arg His Tyr Thr
195          200          205
Asn Ala Ser Asp Gly Leu Cys Thr Arg Leu Ser Arg Pro Cys Gln Thr
210          215          220

```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 6...6
- (D) OTHER INFORMATION: Xaa = Phosphorylated Tyrosine

- (A) NAME/KEY: Other
- (B) LOCATION: 17...17
- (D) OTHER INFORMATION: Xaa = Phosphorylated Tyrosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly Ser Asn Gln Leu Xaa Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
 1 5 10 15
 Xaa Asp Val Leu Asp Lys
 20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GATCGCCATG GGAGTGCAGG TGGAAACCAT CTCCCCA

37

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TACGAATTCT GCGGTGGATC CACGCGGAAC CAGACCTTCC AGTTTTAG

48

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATTAGGATCC ATGCCAGATC CTGCAGCTCA CCTGCCCT

38

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
ATATGGATCC TTACCAGAGG CGTTGCT 27
- (2) INFORMATION FOR SEQ ID NO:13:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
CAATAGGATC CATGGCCAGC AGCGGCATGG CTGA 34
- (2) INFORMATION FOR SEQ ID NO:14:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
GACCTAGGAT CCCTAATTAA CATTTCCCTG TGTGCCGAT 39
- (2) INFORMATION FOR SEQ ID NO:15:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
ATATGGATCC ATGGCGAACA GCCTGGAGCC CGAACCCT 38
- (2) INFORMATION FOR SEQ ID NO:16:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATTAGGATCC TTAGGTCTGG CAGGGGCGGC TCAACCGTGT GCA

43

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 4...4

(D) OTHER INFORMATION: XAA = PHOSPHORYLATED TYROSINE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

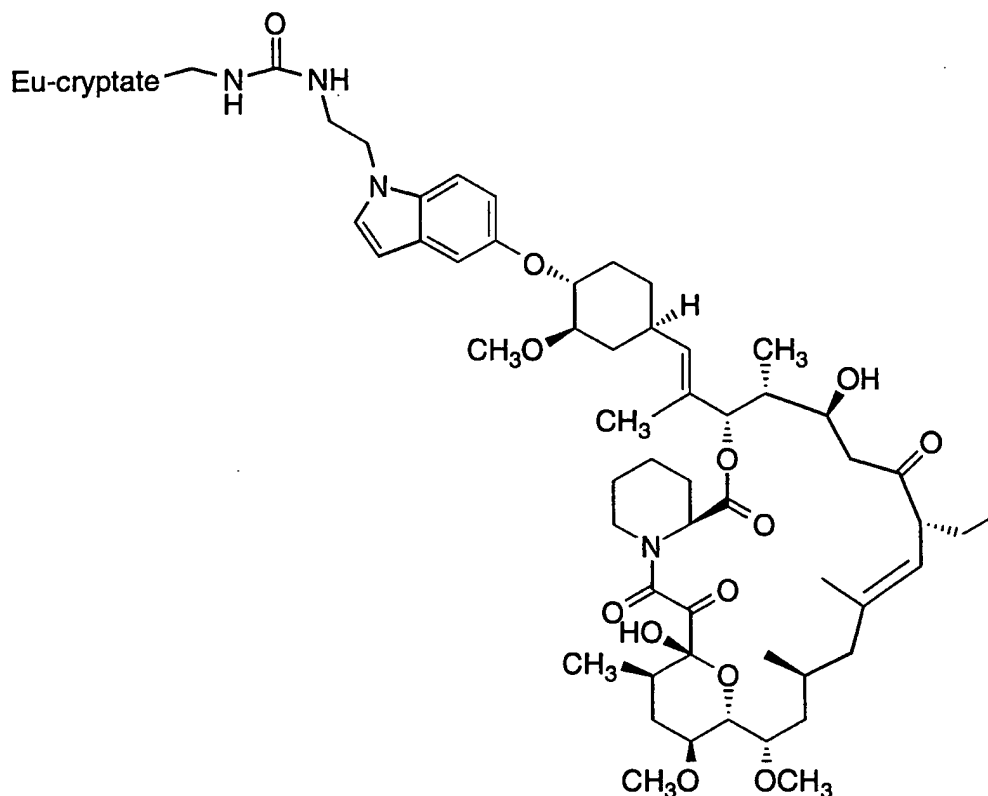
Glu Pro Gln Xaa Glu Glu Ile Pro Ile Tyr Leu
1 5 10

WHAT IS CLAIMED IS:

1. A method of screening for compounds capable of binding to a fusion protein which comprises the steps of:
 - 5 a) mixing a test compound, a biotinylated ligand, the fusion protein, a donor-labeled ligand and acceptor-labeled streptavidin;
 - b) incubating the mixture for a suitable time period;
 - 10 c) measuring the time-resolved fluorescence attributable to the binding of the biotinylated ligand to the fusion protein in the presence of the test compound; and
 - d) determining the binding of the biotinylated ligand to the fusion protein in the presence of the test compound relative to a control assay run in the absence of the test compound.
- 15 2. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 1, wherein the acceptor-labeled streptavidin consists of streptavidin coupled to a light harvesting molecule.
- 20 3. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 2, wherein the acceptor-labeled streptavidin consists of SA-XL665.
- 25 4. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 3, wherein the donor-labeled ligand comprises a cryptate-containing molecule coupled to a lanthanide metal.
- 30 5. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 4, wherein the donor-labeled ligand is selected from the group consisting of a Eu(K)-labeled analog of FK506 or and Eu(K)-labeled analog of rapamycin.

6. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 5, wherein the donor-labeled ligand is an Eu(K)-labeled analog of FK506.

5 7. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 6, wherein the donor-labeled ligand is



8. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 7, wherein the fusion protein comprises an FK506 binding protein, peptide linker and target protein.

9. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 8, wherein the FK506 binding protein is 12kDA human FK506 binding protein.

10. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 9, wherein the target protein is selected from tyrosine phosphatases, nuclear receptors,
5 bacterial tRNA synthetases or single and multiple signal transduction domains.

11. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 10, wherein the target
10 protein comprises a single or multiple signal transduction domain.

12. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 11, wherein the single or multiple signal transduction domain is selected from the group
15 consisting of: SH1, SH2, SH3 and PH domains.

13. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 12, wherein the target protein is a single or multiple SH2 domain.
20

14. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 13, wherein the target protein is a single or multiple SH2 domain selected from the group consisting of: ZAP70:SH2, Syk:SH2 and Lck:SH2.
25

15. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 14, wherein the target protein is the SH2 domain, ZAP70:SH2.

16. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 14, wherein the target protein is the SH2 domain, Syk:SH2.
30

17. The method of screening for compounds capable of binding to a fusion protein, as recited in Claim 14, wherein the target protein is the SH2 domain, Lck:SH2.

5 18. A method of screening for compounds capable of inhibiting a protease which comprises the steps of:

- a) mixing a test compound, a fusion protein substrate, a donor-labeled ligand, acceptor-labeled streptavidin, and a protease;
- 10 b) incubating the mixture for an appropriate time;
- c) measuring the time-resolved fluorescence attributable to the binding of the intact fusion protein substrate to the acceptor-labeled streptavidin in the presence of the test compound; and
- 15 d) determining the binding of the intact fusion protein substrate to the acceptor-labeled streptavidin in the presence of the test compound relative to a control assay run in the absence of the test compound.

20 19. The method of screening for compounds capable of inhibiting a protease, as recited in Claim 18, wherein the protease is selected from the group consisting of thrombin, HIV or TNF α converting enzyme.

25 20. The method of screening for compounds capable of inhibiting a protease, as recited in Claim 19, wherein the protease is thrombin.

30 21. The method of screening for compounds capable of inhibiting a protease, as recited in Claim 20, wherein the acceptor-labeled streptavidin consists of streptavidin coupled to a light harvesting molecule.

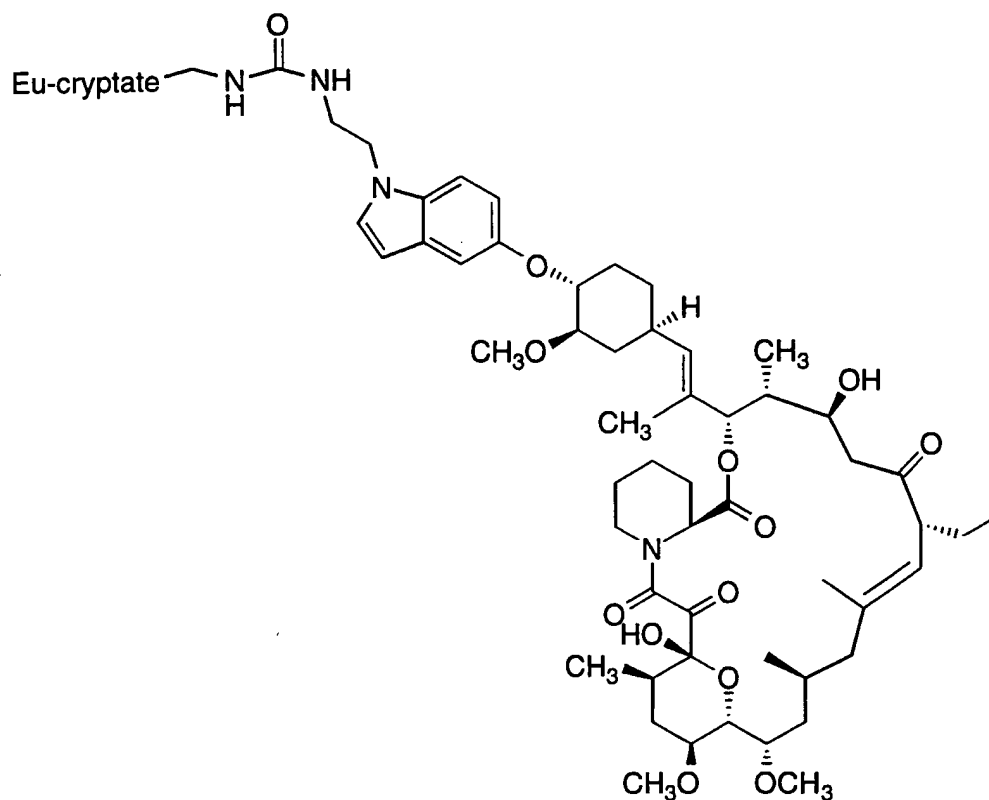
22. The method of screening for compounds capable of inhibiting a protease, as recited in Claim 21, wherein the acceptor-labeled streptavidin consists of SA-XL665.

5 23. The method of screening for compounds capable of inhibiting a protease, as recited in Claim 22, wherein the donor-labeled ligand comprises a cryptate-containing molecule coupled to a lanthanide metal.

10 24. The method of screening for compounds capable of inhibiting a protease, as recited in Claim 23, wherein the donor-labeled ligand is selected from the group consisting of an Eu(K)-labeled analog of FK506 or and Eu(K)-labeled analog of rapamycin.

15 25. The method of screening for compounds capable of inhibiting a protease, as recited in Claim 24, wherein the donor-labeled ligand is an Eu(K)-labeled analog of FK506.

20 26. The method of screening for compounds capable of inhibiting a protease, as recited in Claim 25, wherein the donor-labeled ligand is



27. The method of screening for compounds capable of inhibiting a protease, as recited in Claim 26, wherein the fusion protein comprises an FK506 binding protein, peptide linker and reporter protein.

28. The method of screening for compounds capable of inhibiting a protease, as recited in Claim 27, wherein the FK506 binding protein is 12kDA human FK506 binding protein.

29. The method of screening for compounds capable of inhibiting a protease, as recited in Claim 28, wherein the reporter protein is selected from the group consisting of SH2 domains or covalently biotinylated proteins.

30. The method of screening for compounds capable of inhibiting a protease, as recited in Claim 29, wherein the covalently biotinylated protein is selected from the group consisting of the C-terminal 87 residues of the biotin carboxy carrier protein of acetyl-CoA
5 carboxylase from *Escherichia coli* or the biotin-carrier subunit of transcarboxylase from *Propionibacterium shermanii*.

31. The method of screening for compounds capable of inhibiting a protease, as recited in Claim 29, wherein the SH2 domain is
10 the ZAP70 bound to a biotinylated phosphopeptide derived from an ITAM sequence.

32. The method of screening for compounds capable of inhibiting a protease, as recited in Claim 31, wherein the ITAM
15 sequence is selected from the group consisting of the human T-cell receptor, the B-cell receptor or a high affinity IgE receptor.

33. The method of screening for compounds capable of inhibiting a protease, as recited in Claim 32, wherein the ITAM
20 sequence is the Zeta 1 sequence of the human T-cell receptor. (SEQ. ID. NO. 8)

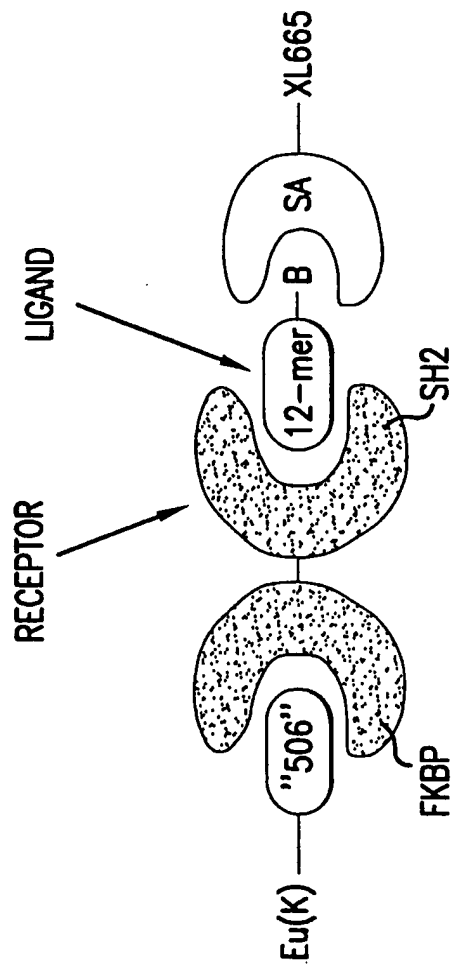


FIG. 1

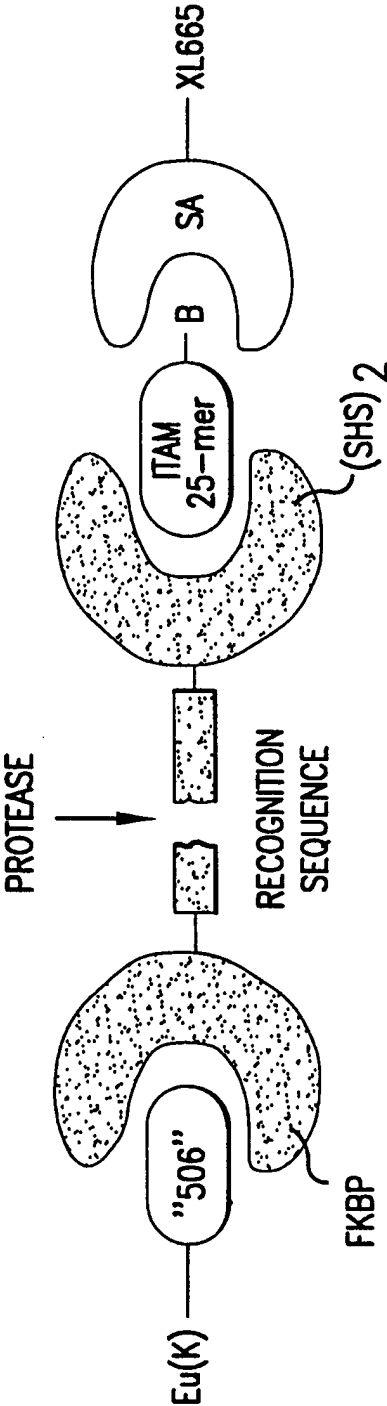


FIG.2

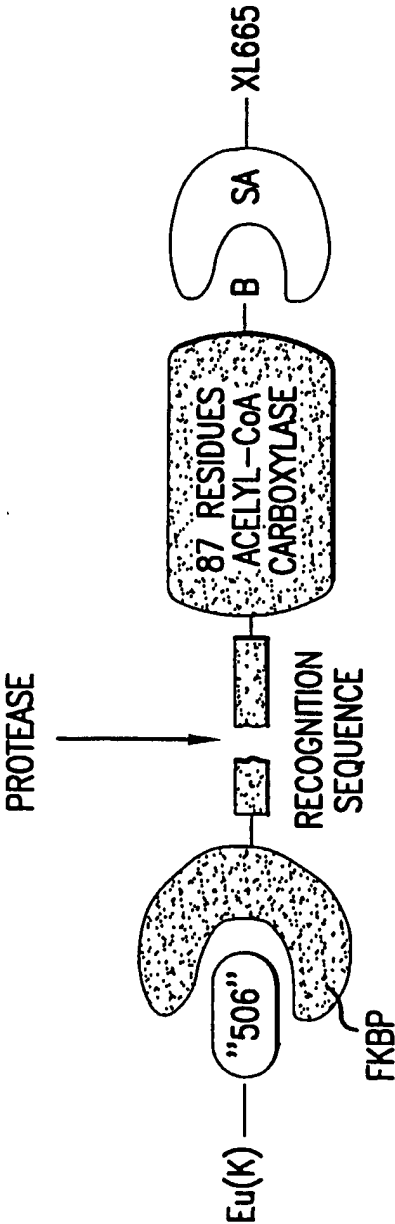


FIG.3

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/04610

A. CLASSIFICATION OF SUBJECT MATTER IPC(6) :G01N 33/53, 33/544, 33/531 US CL :435/7.1, 7.5; 436/529, 543 According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) U.S. : 435/7.1, 7.5; 436/543 Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) APS, DIALOG, GENBANK, BIOTECHDS, BIOSIS, CA, MEDLINE, LIFESCI		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X,P	WO 97/10502 A1 (MERCK & CO., INC.) 20 March 1997, see entire document.	1-33
A	US 5,498,597 A (BURAKOFF et al) 12 March 1996, see entire document.	1-33
A	US 5,352,660 A (PAWSON) 04 October 1994, see entire document.	1-33
<input type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.		
A	Special categories of cited documents: document defining the general state of the art which is not considered to be of particular relevance	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
B	earlier document published on or after the international filing date	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
L	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
O	document referring to an oral disclosure, use, exhibition or other means	
P	document published prior to the international filing date but later than the priority date claimed	*A* document member of the same patent family
Date of the actual completion of the international search 21 MAY 1998		Date of mailing of the international search report 16 JUL 1998
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